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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/964,994

DATE: 01/23/2002
TIME: 09:44:51

Input Set : A:\P3121R1.txt
Output Set: N:\CRF3\01222002\I964994.raw

3 <110> APPLICANT: Goddard,Audrey
4 Godowski,Paul J.
5 Gurney,Austin L.
6 Watanabe,Colin K.
7 Wood,William I.
9 <120> TITLE OF INVENTION: NOVEL POLYPEPTIDES HAVING SEQUENCE SIMILARITY TO
10 CYTOKINE RECEPTORS AND NUCLEIC ACIDS ENCODING THE SAME
12 <130> FILE REFERENCE: P3121R1
14 <140> CURRENT APPLICATION NUMBER: US 09/964,994
15 <141> CURRENT FILING DATE: 2001-09-26
17 <150> PRIOR APPLICATION NUMBER: PCT/US00/08439
18 <151> PRIOR FILING DATE: 2000-03-30
20 <150> PRIOR APPLICATION NUMBER: PCT/US01/06520
21 <151> PRIOR FILING DATE: 2001-02-28
23 <150> PRIOR APPLICATION NUMBER: US 60/191,015
24 <151> PRIOR FILING DATE: 2000-03-21
26 <150> PRIOR APPLICATION NUMBER: US 09/941,992
27 <151> PRIOR FILING DATE: 2001-08-28
29 <160> NUMBER OF SEQ ID NOS: 7
31 <210> SEQ ID NO: 1
32 <211> LENGTH: 1318
33 <212> TYPE: DNA
34 <213> ORGANISM: Homo Sapien
36 <400> SEQUENCE: 1
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39 cttccataaga ggattaacaa agacaaaata tggaaaaaac ataacatggc 100
41 gtcccataat tattagatct tattattgac actaaaaatgg cattaaaatt 150
43 accaaaagga agacagcatc tgtttcctct ttggcctga gctggtaaaa 200
45 aggaacactg gttgcctgaa cagtccacact tgcaaccatg atgcctaaac 250
47 attgctttct aggcttcctc atcagtttct tccttactgg tgttagcagga 300
49 actcagtcaa cgcatgagtc tctgaaggct cagagggtac aatttcagtc 350
51 ccgaaatttt cacaacattt tgcaatggca gcctgggagg gcacttactg 400
53 gcaacagcag tgtctatttt gtgcagtaca aaatcatgtt ctcatgcagc 450
55 atgaaaagct ctcaccagaa gccaaagtggc tgctggcagc acatttcttg 500
57 taacttcca ggctgcagaa cattggctaa atatggacag agacaatgg 550
59 aaaataaaaga agactgttgg ggtactcaag aactctcttg tgaccttacc 600
61 agtggaaacct cagacatataca ggaaccttat tacggggagg tgagggcg 650
63 ctcggctggg agctactcag aatggagacat gacgccgcgg ttcactccct 700
65 ggtggaaac aaaaatagat cctccagtc tgaatataac ccaagtcaat 750
67 ggcttttgtt tggttaattct ccatgctcca aatttaccat atagatacca 800
69 aaaggaaaaa aatgtatcta tagaagatta ctatgaacta ctataccgag 850
71 tttttataat taacaattca ctagaaaagg agcaaaaggt ttatgaaggg 900
73 gctcacagag cggtgaaat tgaagctcta acaccacact ccagctactg 950

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75 tgttagtggct gaaatatatc agcccatgtt agacagaaga agtcagagaa 1000
77 gtgaagagag atgtgtggaa attccatgac ttgtgaaatt tggcatttcag 1050
79 caatgtggaa attctaaagc tccctgagaa caggatgact cgtgtttgaa 1100
81 ggatcttatt taaaattgtt tttgtattt cttaaagcaa tattcaactgt 1150
83 tacaccttgg ggacttctt gtttatccat tctttatcc tttatattc 1200
85 atttgtaaac tatattgaa cgacattccc cccgaaaaat tgaaatgtaa 1250
87 agatgaggca gagaataaaag tggctatga aaaaaaaaaa aaaaaaaaaa 1300
89 aaaaaaaaaa aaaaaaaaa 1318
91 <210> SEQ ID NO: 2
92 <211> LENGTH: 262
93 <212> TYPE: PRT
94 <213> ORGANISM: Homo Sapien
96 <400> SEQUENCE: 2
97 Met Pro Lys His Cys Phe Leu Gly Phe Leu Ile Ser Phe Phe Leu
98 1 5 10 15
100 Thr Gly Val Ala Gly Thr Gln Ser Thr His Glu Ser Leu Lys Pro
101 20 25 30
103 Gln Arg Val Gln Phe Gln Ser Arg Asn Phe His Asn Ile Leu Gln
104 35 40 45
106 Trp Gln Pro Gly Arg Ala Leu Thr Gly Asn Ser Ser Val Tyr Phe
107 50 55 60
109 Val Gln Tyr Lys Ile Met Phe Ser Cys Ser Met Lys Ser Ser His
110 65 70 75
112 Gln Lys Pro Ser Gly Cys Trp Gln His Ile Ser Cys Asn Phe Pro
113 80 85 90
115 Gly Cys Arg Thr Leu Ala Lys Tyr Gly Gln Arg Gln Trp Lys Asn
116 95 100 105
118 Lys Glu Asp Cys Trp Gly Thr Gln Glu Leu Ser Cys Asp Leu Thr
119 110 115 120
121 Ser Glu Thr Ser Asp Ile Gln Glu Pro Tyr Tyr Gly Arg Val Arg
122 125 130 135
124 Ala Ala Ser Ala Gly Ser Tyr Ser Glu Trp Ser Met Thr Pro Arg
125 140 145 150
127 Phe Thr Pro Trp Trp Glu Thr Lys Ile Asp Pro Pro Val Met Asn
128 155 160 165
130 Ile Thr Gln Val Asn Gly Ser Leu Leu Val Ile Leu His Ala Pro
131 170 175 180
133 Asn Leu Pro Tyr Arg Tyr Gln Lys Glu Lys Asn Val Ser Ile Glu
134 185 190 195
136 Asp Tyr Tyr Glu Leu Leu Tyr Arg Val Phe Ile Ile Asn Asn Ser
137 200 205 210
139 Leu Glu Lys Glu Gln Lys Val Tyr Glu Gly Ala His Arg Ala Val
140 215 220 225
142 Glu Ile Glu Ala Leu Thr Pro His Ser Ser Tyr Cys Val Val Ala
143 230 235 240
145 Glu Ile Tyr Gln Pro Met Leu Asp Arg Arg Ser Gln Arg Ser Glu
146 245 250 255
148 Glu Arg Cys Val Glu Ile Pro
149 260

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151 <210> SEQ ID NO: 3
152 <211> LENGTH: 27
153 <212> TYPE: DNA
154 <213> ORGANISM: Artificial Sequence
156 <220> FEATURE:
157 <223> OTHER INFORMATION: Synthetic oligonucleotide probe
159 <400> SEQUENCE: 3
160 ctggcaacag cagtgtctat tttgtgc 27
162 <210> SEQ ID NO: 4
163 <211> LENGTH: 21
164 <212> TYPE: DNA
165 <213> ORGANISM: Artificial Sequence
167 <220> FEATURE:
168 <223> OTHER INFORMATION: Synthetic oligonucleotide probe
170 <400> SEQUENCE: 4
171 taagtgcctt cccaggcgtgc c 21
173 <210> SEQ ID NO: 5
174 <211> LENGTH: 52
175 <212> TYPE: DNA
176 <213> ORGANISM: Artificial Sequence
178 <220> FEATURE:
179 <223> OTHER INFORMATION: Synthetic oligonucleotide probe
181 <400> SEQUENCE: 5
182 tcctccagtc atgaatataaa cccaaagtcaa tggctctttg ttggtaattc 50
184 tc 52
186 <210> SEQ ID NO: 6
187 <211> LENGTH: 1705
188 <212> TYPE: DNA
189 <213> ORGANISM: Homo Sapien
191 <400> SEQUENCE: 6
192 taaaatgact tccacggctg ggacgggaac cttccaccca cagctatgcc 50
194 tctgatttgtt gaatggtgaa ggtgcctgtc taacttttct gtaaaaagaa 100
196 ccagctgcctt ccaggcagcc agccctcaag catcaactac aggaccagag 150
198 ggacaagaca tgactgttat gaggagctgc tttcgccat ttaacaccaa 200
200 gaagaattga ggctgcttgg gaggaaggcc aggaggaaca cgagactgag 250
202 agatgaattt tcaacagagg ctgcaaagcc tgtggacttt agccagaccc 300
204 ttctgccttc ctttgtggc gacagctct caaatgcaga tggttgtgct 350
206 cccttgctgtt ggttttaccc tgcttctctg gagccaggta tcagggccc 400
208 agggccaaga attccacttt gggccctgcc aagtgaagggg ggttgttccc 450
210 cagaaaactgt gggaaacgtt ctgggctgtg aaagacacta tgcaagctca 500
212 ggataacatc acgagtgcctt ggctgtgc gcaggagggtt ctgcagaacg 550
214 tctcgatgc tgagagctgt taccttgtcc acaccctgtt ggagttctac 600
216 ttgaaaactg tttcaaaaaa ccaccacaa ataacagttt aagtctggac 650
218 tctgaagtca ttctctactc tggccaaacaa ctttgttctc atcgtgtcac 700
220 aactgcaacc cagtcagaa aatgagatgt tttccatcag agacagtgc 750
222 cacaggcgggt ttctgttattt ccggagagca ttcaaaacagt tggacgtaga 800
224 agcagctctg accaaagccc ttggggaaat ggacattttt ctgacctgga 850
226 tgcagaaattt ctacaagctc tgaatgtcta gaccaggacc tccctcccc 900
228 tggcacttgtt ttgttccctgt tgcatttca aacagtctcc cttccatgc 950

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230 tgttcactgg acacttcacg cccttggcca tgggtccat tcttggccca 1000
232 ggattattgt caaagaagtc attcttaag cagcgccagt gacagtcagg 1050
234 gaaggtgcct ctggatgctg tgaagagtct acagagaaga ttcttgatt 1100
236 tattacaact ctatttaatt aatgtcaacta ttcaactga agttctattt 1150
238 atttgtgaga ctgttaagtta catgaaggca gcagaatatt gtgcccattg 1200
240 cttcttacc cctcacaatc cttgccacag tgtgggcag tggatgggtg 1250
242 ctttagtaagt acttaataaa ctgtgggtct tttttggcc tgcctttgg 1300
244 ttgttaaaaa acagagaggg atgcttgat gtaaaactga acttcagagc 1350
246 atgaaaatca cactgtcttc tgatatctgc agggacagag cattgggtg 1400
248 ggggttaaggt gcatctgttt gaaaagtaaa cgataaaaatg tggattaaag 1450
250 tgcccagcac aaagcagatc ctcaataaaac atttcatttc ccacccacac 1500
252 tcgcccagctc accccatcat cccttccct tgggccctc cttttttttt 1550
254 tattccttagtc attcttccct aatcttccac ttgagtgatc agctgaccctt 1600
256 gctgatgggtg acattgcacc tggatgtact atccaatctg tgcgtacatt 1650
258 ccctgctaataa aaaaagacaac ataactccaa aaaaaaaaaa 1700
260 aaaaaa 1705
262 <210> SEQ ID NO: 7
263 <211> LENGTH: 206
264 <212> TYPE: PRT
265 <213> ORGANISM: Homo Sapien
267 <400> SEQUENCE: 7
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269 1 5 10 15
271 Pro Phe Cys Pro Pro Leu Leu Ala Thr Ala Ser Gln Met Gln Met
272 20 25 30
274 Val Val Leu Pro Cys Leu Gly Phe Thr Leu Leu Leu Trp Ser Gln
275 35 40 45
277 Val Ser Gly Ala Gln Gly Gln Glu Phe His Phe Gly Pro Cys Gln
278 50 55 60
280 Val Lys Gly Val Val Pro Gln Lys Leu Trp Glu Ala Phe Trp Ala
281 65 70 75
283 Val Lys Asp Thr Met Gln Ala Gln Asp Asn Ile Thr Ser Ala Arg
284 80 85 90
286 Leu Leu Gln Gln Glu Val Leu Gln Asn Val Ser Asp Ala Glu Ser
287 95 100 105
289 Cys Tyr Leu Val His Thr Leu Leu Glu Phe Tyr Leu Lys Thr Val
290 110 115 120
292 Phe Lys Asn His His Asn Arg Thr Val Glu Val Arg Thr Leu Lys
293 125 130 135
295 Ser Phe Ser Thr Leu Ala Asn Asn Phe Val Leu Ile Val Ser Gln
296 140 145 150
298 Leu Gln Pro Ser Gln Glu Asn Glu Met Phe Ser Ile Arg Asp Ser
299 155 160 165
301 Ala His Arg Arg Phe Leu Leu Phe Arg Arg Ala Phe Lys Gln Leu
302 170 175 180
304 Asp Val Glu Ala Ala Leu Thr Lys Ala Leu Gly Glu Val Asp Ile
305 185 190 195
307 Leu Leu Thr Trp Met Gln Lys Phe Tyr Lys Leu
308 200 205

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